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RAW SEQUENCE LISTING

DATE: 03/27/2002

PATENT APPLICATION: US/09/734,237B

TIME: 13:30:20

Input Set : A:\B583\_40608.txt

Output Set: N:\CRF3\03272002\I734237B.raw

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3 <110> APPLICANT: Rozzell, J. David
4     Bui, Peter
5     Hua, Ling
7 <120> TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION
9 <130> FILE REFERENCE: B583:40608
11 <140> CURRENT APPLICATION NUMBER: US 09/734,237B
12 <141> CURRENT FILING DATE: 2000-12-08
14 <150> PRIOR APPLICATION NUMBER: 09/494,921
15 <151> PRIOR FILING DATE: 2000-01-31
17 <160> NUMBER OF SEQ ID NOS: 79
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1197
23 <212> TYPE: DNA
24 <213> ORGANISM: Pseudomonas putida
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27 atgcacggct ccaacaagct cccaggattt gccacccgag ccattcacca tggctacgac      60
29 ccccaggacc acggcggcgc actggtgcca ccggtctacc agaccgagac gttcaccttc      120
31 cccaccgtgg aatacggcgc tgcgtgcttt gccggcgagc aggccgggca tttctacagc      180
33 cgcattctca accccaccct caacctgctg gaagcacgca tggcctcgct ggaaggcggc      240
35 gaggcggggc tggcgctggc ctcgggcatg ggggcgatca cgtccacgct atggacactg      300
37 ctgcgccccg gtgacgaggt gctgctgggc aacaccctgt acggctgcac ctttgccttc      360
39 ctgcaccacg gcatcggcga gttcgggggtc aagctgcgcc atgtggacat ggccgacctg      420
41 caggcactgg aggcggccat gacgcgggcc acccggggtga tctatttcga gtcgcccggc      480
43 aaccccaaca tgcacatggc cgatatcgcc ggcgtggcga agattgcacg caagcacggc      540
45 gcgaccgtgg tggtcgacaa cacctactgc acgcccgtacc tgcaacggcc actggagctg      600
47 ggcgcccacc tgggtggtgca ttcggccacc aagtacctga ggcggccatgg cgacatcact      660
49 gctggcattg tgggtggcag ccaggcactg gtggaccgta tacgtctgca gggcctcaag      720
51 gacatgaccg gtgcggtgct ctgcgcccat gacgcgcgac tgttgatgag cggcatcaag      780
53 accctcaacc tgcgcatgga ccgccaactg gccaacgctc aggtgctggc cgagttcttc      840
55 gcccggcagc cgcaggtgga gctgatccat taccggggcc tggcgagctt cccgcagtac      900
57 accctggccc gccagcagat gagccagccg ggcggcatga tcgccttcga actcaagggc      960
59 ggcattcggt ccgggcggcg gttcatgaac gccctgcaac tgttcagccg cgcgggtgagc      1020
61 ctggggcgat ccgagtcgct ggcgcagcac ccggcaagca tgactcattc cagctatacc      1080
63 ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tgcggttgtc ggtggggctg      1140
65 gaagacatcg acgacctgct ggccgatgtg caacaggcac tcaaggcgag tgcctga      1197
68 <210> SEQ ID NO: 2
69 <211> LENGTH: 399
70 <212> TYPE: PRT
71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: Pseudomonas putida methionine gamma-lyase amino acid
sequence, w
75     ith a non-naturally occurring glycine residue inserted at positio

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76      n 2
78 <400> SEQUENCE: 2
80 Met Gly His Gly Ser Asn Lys Leu Pro Gly Phe Ala Thr Arg Ala Ile
81 1      5      10      15
84 His His Gly Tyr Asp Pro Gln Asp His Gly Gly Ala Leu Val Pro Pro
85      20      25      30
88 Val Tyr Gln Thr Ala Thr Phe Thr Phe Pro Thr Val Glu Tyr Gly Ala
89      35      40      45
92 Ala Cys Phe Ala Gly Glu Gln Ala Gly His Pro Tyr Ser Arg Ile Ser
93      50      55      60
96 Asn Pro Thr Leu Asn Leu Leu Gln Ala Arg Met Ala Ser Leu Glu Gly
97 65      70      75      80
100 Gly Glu Ala Gly Leu Ala Leu Ala Ser Gly Met Gly Ala Ile Thr Ser
101      85      90      95
104 Thr Leu Tyr Thr Leu Leu Arg Pro Gly Asp Glu Val Leu Leu Gly Asn
105      100      105      110
108 Thr Leu Tyr Gly Cys Thr Phe Ala Phe Leu His His Gly Ile Gly Glu
109      115      120      125
112 Phe Gly Val Lys Leu Arg His Val Asp Met Ala Asp Leu Gln Ala Leu
113      130      135      140
116 Glu Ala Ala Met Thr Pro Ala Thr Arg Val Ile Tyr Phe Glu Ser Pro
117 145      150      155      160
120 Ala Asn Pro Asn Met His Met Ala Asp Ile Ala Gly Val Ala Lys Ile
121      165      170      175
124 Ala Arg Lys His Gly Ala Thr Val Val Val Asp Asn Thr Tyr Cys Thr
125      180      185      190
128 Pro Tyr Leu Gln Arg Pro Leu Gln Leu Gly Ala Asp Leu Val Val His
129      195      200      205
132 Ser Ala Thr Lys Tyr Leu Ser Gly His Gly Asp Ile Thr Ala Gly Ile
133      210      215      220
136 Val Val Gly Ser Gln Ala Leu Val Asp Arg Ile Arg Leu Gln Gly Leu
137 225      230      235      240
140 Lys Asp Met Thr Gly Ala Val Leu Ser Pro His Asp Ala Ala Leu Leu
141      245      250      255
144 Met Arg Gly Ile Lys Thr Leu Asn Leu Arg Met Asp Arg His Cys Ala
145      260      265      270
148 Asn Ala Gln Val Leu Ala Glu Phe Leu Ala Arg Gln Pro Gln Val Glu
149      275      280      285
152 Leu Ile His Tyr Pro Gly Leu Ala Ser Phe Pro Gln Tyr Thr Leu Ala
153      290      295      300
156 Arg Gln Gln Met Ser Gln Pro Gly Gly Met Ile Ala Phe Glu Leu Lys
157 305      310      315      320
160 Gly Gly Ile Gly Ala Gly Arg Arg Phe Met Asn Ala Leu Gln Leu Phe
161      325      330      335
164 Ser Arg Ala Val Ser Leu Gly Asp Ala Glu Ser Leu Ala Gln His Pro
165      340      345      350
168 Ala Ser Met Thr His Ser Ser Tyr Thr Pro Glu Glu Arg Ala His Tyr
169      355      360      365
172 Gly Ile Ser Glu Gly Leu Val Arg Leu Ser Val Gly Leu Glu Asp Ile

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173      370      375      380
176 Asp Asp Leu Leu Ala Asp Val Gln Gln Ala Leu Lys Ala Ser Ala
177 385      390      395
180 <210> SEQ ID NO: 3
181 <211> LENGTH: 1202
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Pseudomonas putida methionine gamma-lyase sequence, with
glycine
187      codon inserted to incorporate restriction site and numerous natur
188      ally occurring codons changed to codons more commonly used in ent
189      eric bacteria
191 <400> SEQUENCE: 3
192 catgggtcac ggctccaaca aactgccggg ctttgctacc cgcgctatcc accacggtta      60
194 tgacccgcag gatcacggtg gtgcaactgg tccgccgggt taccagactg ctactttcac      120
196 ctccccgacc gttgaatacg gcgctgcgtg ctttgctggc gaacaggctg gtcacttcta      180
198 ctcccgatc tccaaccgga ccctgaacct gctggaagca cgtatggcat ctctggaagg      240
200 cggcgaagct ggtctggcgc tggcatctgg tatgggcgcg atcacctcta ccctgtggac      300
202 cctgctgcgt ccgggtgacg aagttctgct gggcaacacc ctgtatggtt gtacttttgc      360
204 tttcctgcac cacggtatcg gtgaattcgg cgtaaactg cgtcacgtag atatggctga      420
206 cctgcaggca ctggaagcgg ctatgacccc ggctaccggt gttatctact tcgaatcccc      480
208 ggctaaccgc aacatgcaca tggctgacat cgcagggtgt gctaaaatcg ctcgtaagca      540
210 cggcgctacc gtagtgtgtg ataacacct ctgtaactcg tacctgcaac gtccgctgga      600
212 actgggcgct gacctggttg ttcaactcgc tactaaatac ctgtccggcc acggcgacat      660
214 cactgctggc atcgtagtag gctcccaggc actggttgac cgtatccgtc tgcaaggctc      720
216 gaaagacatg accggcgctg ttctgtcccc gcacgacgca gcaactgctga tgcgtggtat      780
218 caagaccctg aacctgcgta tggaccgtca ctgtgctaac gctcaggtag tggctgaatt      840
220 cctggctcgt cagccgcagg tagaactgat ccaactatcc ggcctggctt ccttcccgca      900
222 gtacactctg gcacgtcagc agatgtccca gccgggcggt atgatcgctt tcgaactgaa      960
224 ggggtggcatc ggcgctggtc gtcgtttcat gaacgctctg cagctgttct cccgtgcggt      1020
226 ttccctgggt gacgctgaat ccctggcgca gcaaccggca tccatgactc actcctccta      1080
228 cactccggaa gaacgtgcgc actacggcat ctccgaaggc ctgggttcgtc tgtctgttgg      1140
230 tctggaagac atcgatgata tgctggcaga cgttcagcag gctctgaagg ctagecgttg      1200
232 ag      1202
235 <210> SEQ ID NO: 4
236 <211> LENGTH: 426
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Cloning fragment of SEQ ID NO. 3
243 <400> SEQUENCE: 4
244 catgggtcac ggctccaaca aactgccggg ctttgctacc cgcgctatcc accacggtta      60
246 tgacccgcag gatcacggtg gtgcaactgg tccgccgggt taccagactg ctactttcac      120
248 ctccccgacc gttgaatacg gcgctgcgtg ctttgctggc gaacaggctg gtcacttcta      180
250 ctcccgatc tccaaccgga ccctgaacct gctggaagca cgtatggcat ctctggaagg      240
252 cggcgaagct ggtctggcgc tggcatctgg tatgggcgcg atcacctcta ccctgtggac      300
254 cctgctgcgt ccgggtgacg aagttctgct gggcaacacc ctgtatggtt gtacttttgc      360
256 tttcctgcac cacggtatcg gtgaattcgg cgtaaactg cgtcacgtag atatggctga      420
258 cctgca      426

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261 <210> SEQ ID NO: 5
262 <211> LENGTH: 441
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Cloning fragment of SEQ ID NO. 3
269 <400> SEQUENCE: 5
270 caagaggcca tgggtcacgg ctccaacaaa ctgccgggct ttgctaccgg cgctatccac      60
272 cacggttatg acccgcagga tcacggtggt gcactggttc cgccgggtta ccagactgct      120
274 actttcacct tcccgaccgt tgaatacggc gctgcggtgt ttgctggcga acaggctggt      180
276 cacttctact cccgtatctc caaccggacc ctgaacctgc tgggaagcac tatggcatct      240
278 ctggaaggcg gcgaagctgg tctggcgctg gcatctggta tgggcgcgat cacctctacc      300
280 ctgtggacct tgctgcgtcc gggtgacgaa gttctgctgg gcaacaccct gtatggttgt      360
282 acttttgctt tcctgcacca cggtatcggt gaattcggcg ttaaactgcg tcacgtagat      420
284 atggctgacc tgcaggcact g
287 <210> SEQ ID NO: 6
288 <211> LENGTH: 410
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Cloning fragment of SEQ ID NO. 3
295 <400> SEQUENCE: 6
296 ggcactggaa gcggctatga ccccggttac ccgtgttata tacttcgaat ccccggttaa      60
298 cccgaacatg cacatggctg acatgcgagg tgttgctaaa atcgctcgta agcacggcgc      120
300 taccgtagtt gttgataaca cctactgtac tccgtacctg caacgtccgc tggaaactggg      180
302 cgctgacctg gttgttcaat ccgtactata atacctgtcc ggccacggcg acatcactgc      240
304 tggcatcgta gtaggctccc aggcactggt tgacctatc cgtctgcaag gtctgaaaga      300
306 catgaccggc gctgttctgt ccccgcacga cgcagcactg ctgatgcgtg gtatcaagac      360
308 cctgaacctg cgtatggacc gtcactgtgc taacgctcag gtactggctg
311 <210> SEQ ID NO: 7
312 <211> LENGTH: 430
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Cloning fragment of SEQ ID NO. 3
319 <400> SEQUENCE: 7
320 gctgacctgc aggcactgga agcggctatg accccggcta cccgtgttat ctacttcgaa      60
322 tcccgggcta acccgaacat gcacatggct gacatcgag gtgttgctaa aatcgctcgt      120
324 aagcacggcg ctaccgtagt tggtgataac acctactgta ctccgtacct gcaacgtccg      180
326 ctggaactgg gcgctgacct ggttggttac tccgtacta aatacctgtc cggccacggc      240
328 gacatcactg ctggcatcgt agtaggctcc caggcactgg ttgacctat ccgtctgcaa      300
330 ggtctgaaag acatgaccgg cgctgttctg tcccgcacg acgcagcact gctgatgcgt      360
332 ggtatcaaga ccctgaacct gcgtatggac cgtcactgtg ctaacgctca ggtactggct      420
334 gaattcctgg
337 <210> SEQ ID NO: 8
338 <211> LENGTH: 366
339 <212> TYPE: DNA
340 <213> ORGANISM: Artificial sequence
342 <220> FEATURE:

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343 <223> OTHER INFORMATION: Cloning fragment of SEQ ID NO. 3
345 <400> SEQUENCE: 8
346 aattcctggc tcgtcagccg caggtagaac tgatccacta tccgggacctg gcttccttcc      60
348 cgcagtacac tctggcacgt cagcagatgt cccagccggg cggtatgata gctttcgaac      120
350 tgaagggtgg catcgccgct ggtcgtcgtt tcatgaacgc tctgcagctg ttctcccgctg      180
352 cggtttccct gggtgacgct gaatccctgg cgcagcaccg ggcattccatg actcactcct      240
354 cctacactcc ggaagaacgt gcgcactacg gcatctccga aggcctgggt cgtctgtctg      300
356 ttggtctgga agacatcgat gatctgctgg cagacgttca gcaggctctg aaggctagcg      360
358 cttgag                                           366
361 <210> SEQ ID NO: 9
362 <211> LENGTH: 383
363 <212> TYPE: DNA
364 <213> ORGANISM: Artificial sequence
366 <220> FEATURE:
367 <223> OTHER INFORMATION: Cloning fragment of SEQ ID NO. 3
369 <400> SEQUENCE: 9
370 tcttaatgaa ttcttggtc gtcagccgca ggtagaactg atccactatc cgggcctggc      60
372 ttcttcccg cagtacactc tggcacgtca gcagatgtcc cagccgggcg gtatgatcgc      120
374 ttctgaactg aagggtggca tcggcgctgg tcgtcgtttc atgaacgctc tgcagctggt      180
376 ctcccgctgc gtttccttgg gtgacgctga atccctggcg cagcaccgcg catccatgac      240
378 tcaactctcc tacactccgg aagaacgtgc gcactacggc atctccgaag gcctggttcg      300
380 tctgtctgtt ggtctggaag acatcgatga tctgctggca gacgttcagc aggctctgaa      360
382 ggctagcgtc tgaggatcca cca                                           383
385 <210> SEQ ID NO: 10
386 <211> LENGTH: 33
387 <212> TYPE: DNA
388 <213> ORGANISM: Artificial Sequence
390 <220> FEATURE:
391 <223> OTHER INFORMATION: Primer/template derived from SEQ ID NO. 3
393 <400> SEQUENCE: 10
394 caagaggcca tgggtcacgg ctccaacaaa ctg                                           33
397 <210> SEQ ID NO: 11
398 <211> LENGTH: 114
399 <212> TYPE: DNA
400 <213> ORGANISM: Artificial Sequence
402 <220> FEATURE:
403 <223> OTHER INFORMATION: Primer/template derived from SEQ ID NO. 3
405 <400> SEQUENCE: 11
406 cagcgtcca acaaactgcc gggctttgct acccgcgcta tccaccacgg ttatgaccgg      60
408 caggatcacg gtggtgcact ggttcgcgcg gtttaccaga ctgctacttt cacc      114
411 <210> SEQ ID NO: 12
412 <211> LENGTH: 116
413 <212> TYPE: DNA
414 <213> ORGANISM: Artificial Sequence
416 <220> FEATURE:
417 <223> OTHER INFORMATION: Primer/template derived from SEQ ID NO. 3
419 <400> SEQUENCE: 12
420 gcttcagca ggttcagggc cggggttgag atacgggagt agaagtgacc agcctgttcg      60
422 ccagcaaagc acgcagcgcc gtattcaacg gtcgggaagg tgaaagtagc agtctg      116

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